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     (FILE 'HOME' ENTERED AT 20:14:25 ON 07 DEC 2001)

     FILE 'MEDLINE, SCISEARCH, LIFESCI, BIOTECHDS, BIOSIS, EMBASE, HCAPLUS,
     NTIS, ESBIOBASE, BIOTECHNO, WPIDS' ENTERED AT 20:14:34 ON 07 DEC 2001
L1             0 S AMYLASE (5A) LICHNIFORMIS
L2          1659 S AMYLASE (5A) LICHENIFORMIS
L3            95 S AMYLASE (5A) LICHENIFORMIS (5A) MUTA?
L4            30 S AMYLASE (5A) LICHENIFORMIS (10A) MUTAT?
L5            28 S AMYLASE (5A) LICHENIFORMIS (5A) MUTAT?
L6           233 S L2 AND MUTA?
L7             9 S L6 AND 11
L8             8 DUP REM L7 (1 DUPLICATE REMOVED)
L9             7 S L6 AND 16
L10            5 S L9 NOT L8
L11            7 DUP REM L9 (0 DUPLICATES REMOVED)
L12            5 S L11 NOT L8
L13            2 S L6 AND 49
L14            2 S L13 NOT L8
L15            0 S L6 AND 84
L16            1 S L6 AND 144
L17            0 S L6 AND 167
L18            0 S L6 AND 169
L19            9 S L6 AND 178
L20            5 S L10 NOT L8
L21            9 S L19 NOT L8
L22            2 DUP REM L21 (7 DUPLICATES REMOVED)
L23            3 S L6 AND 188
L24            2 DUP REM L23 (1 DUPLICATE REMOVED)
L25            9 S L6 AND 190
L26            2 DUP REM L25 (7 DUPLICATES REMOVED)
L27            1 S L6 AND 205
L28           25 S L6 AND 209
L29            8 DUP REM L28 (17 DUPLICATES REMOVED)

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COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                   115.00     115.15

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)          SINCE FILE      TOTAL
                                                       ENTRY    SESSION
CA SUBSCRIBER PRICE                                    -5.29      -5.29

 SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 20:46:02 ON 07 DEC 2001
```

'ANSWER 2 OF 2 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI Amino acid residues stabilizing a Bacillus alpha-amylase against irreversible thermoinactivation;
enzyme engineering by site directed **mutagenesis** and chimeric gene construction with Bacillus **licheniformis** and Bacillus amyloliquefaciens alpha-**amylase** gene
AB The thermostable alpha-**amylase** of Bacillus **licheniformis** retains 80% of its activity at 90 deg for 30 min and has a temp. optimum of 80-85 deg. Chimeric genes were constructed for alpha-**amylase** using genes derived from B. **licheniformis** and Bacillus amyloliquefaciens. The stability of the constructs was determined. Regions I (Gln-**178**) and II (255th-270th residues) of B. **licheniformis** alpha-**amylase** gene played a major role in thermostability. The alpha-**amylase** genes derived from B. **licheniformis** and B. amyloliquefaciens were subjected to site-directed **mutagenesis** to determine which regions are required for enhancement of thermostability. Deletion of Arg-176 and Gly-177 in region I and substitutions. . . of Ala for Lys-269 and Asp for Asn-266 in region II of the B. amyloliquefaciens alpha-amylase gene enhanced thermostability. The **mutant** enzymes were thermostable like the B. licheniformis enzyme but had temp. optima similar to the enzymes derived from B. amyloliquefaciens. These **mutant** enzymes were susceptible to reversible inactivation at temp. above 65 deg. (26 ref)
CT BACILLUS **LICHENIFORMIS** BACILLUS AMYLOLIQUEFACIENS THERMOSTABLE ALPHA-**AMYLASE** ENZYME ENGINEERING PROTEIN ENGINEERING EC-3.2.1.1 BACTERIUM CLONING

=> d l22

L22 ANSWER 1 OF 2 MEDLINE DUPLICATE 1
AN 2000438427 MEDLINE
DN 20425100 PubMed ID: 10966804
TI Probing structural determinants specifying high thermostability in Bacillus **licheniformis** alpha-**amylase**.
AU Declerck N; Machius M; Wiegand G; Huber R; Gaillardin C
CS Genetique Moleculaire et Cellulaire, INRA-UMR216 and CNRS-URA1925 INA-PG, Thiverval-Grignon, F-78850, France.. nathalie@tome.cbs.univ-montpl.fr
SO JOURNAL OF MOLECULAR BIOLOGY, (2000 Aug 25) 301 (4) 1041-57.
Journal code: J6V; 2985088R. ISSN: 0022-2836.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200009
ED Entered STN: 20000928
Last Updated on STN: 20000928
Entered Medline: 20000921

=> d l22 2

L22 ANSWER 2 OF 2 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
AN 1990-00500 BIOTECHDS
TI Amino acid residues stabilizing a Bacillus alpha-amylase against irreversible thermoinactivation;
enzyme engineering by site directed **mutagenesis** and chimeric gene construction with Bacillus **licheniformis** and Bacillus amyloliquefaciens alpha-**amylase** gene
AU Suzuki Y; Ito N; Yuuki T; *Yamagata H; Udaka S
LO Department of Food Science and Technology, Faculty of Agriculture, Nagoya University, Chikusa-ku, Nagoya 464, Japan.
SO J.Biol.Chem.; (1989) 264, 32, 18933-38
CODEN: JBCHA3
DT Journal
LA English

' ANSWER 2 OF 2 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION
AN 1996-03039 BIOTECHDS
TI **Mutant** B. **licheniformis** alpha-**amylase** enzymes;
Bacillus licheniformis **mutant** thermostable enzyme production; application in starch degradation, textile or paper desizing, brewing industry and as household surfactant
AU van der Laan J M; Aehle W
PA Brocades
LO Delft, The Netherlands.
PI WO 9535382 28 Dec 1995
AI WO 1995-EP1688 2 May 1995
PRAI EP 1994-201740 17 Jun 1994
DT Patent
LA English
OS WPI: 1996-058419 [06]

=> d 2 kwic

L24 ANSWER 2 OF 2 BIOTECHDS COPYRIGHT 2001 DERWENT INFORMATION LTD
TI **Mutant** B. **licheniformis** alpha-**amylase** enzymes;
Bacillus licheniformis **mutant** thermostable enzyme production; application in starch degradation, textile or paper desizing, brewing industry and as household surfactant
AB An amylolytic enzyme (I) derived from Bacillus **licheniformis** alpha-**amylase** (EC-3.2.1.1) (or an enzyme with 70% identity) is new, containing 1 or more amino acid changes at position 104 (Asn to Asp), 128 (Val to Glu), 187 (Ser to Asp) and **188** (Asn to Asp) of the wild-type enzyme. Also claimed are: a nucleic acid encoding (I); a vector for the expression. . . detergent composition containing (I). (I) preferably has an additional amino acid change, providing the enzyme with increased thermostability, preferably the **mutations** His 133 to Tyr 133 and Thr 149 to Ile 149. (I) may also have at least 1 amino acid. . . the enzyme with improved oxidation stability, preferably by changing a Met residue to another amino acid, e.g. Met 197. The **mutant** enzyme has higher activity under optimal and suboptimal conditions (pH less than 6.5 or over 7 and/or Ca2+ concentration under. . .
CT BACILLUS **LICHENIFORMIS MUTANT** RECOMBINANT THERMOSTABLE ALPHA-**AMYLASE** PREP., APPL. STARCH DEGRADATION, TEXTILE, PAPER DESIZING, BREWING IND., SURFACTANT COMP. BACTERIUM ENZYME ENGINEERING PROTEIN ENGINEERING EC-3.2.1.1 POLYSACCHARIDE DNA SEQUENCE.

WEST

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Search Results -

Terms	Documents
139 not 14	0

Database: US Patents Full-Text Database; US Pre-Grant Publication Full-Text Database; JPO Abstracts Database; EPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Refine Search: `139 not 14` Clear

Search History

Today's Date: 12/7/2001

DB Name	Query	Hit Count	Set Name
USPT	139 not 14	0	L40
USPT	14 and 209	14	L39
USPT	136 not 14	0	L38
USPT	14 and 205	14	L37
USPT	135 not 14	0	L36
USPT	14 and 190	11	L35
USPT	132 not 14	0	L34
USPT	132 not 14	0	L33
USPT	14 and 188	9	L32
USPT	130 not 14	0	L31
USPT	14 and 178	17	L30
USPT	14 and 169	3	L29
USPT	127 not 14	0	L28
USPT	14 and 167	8	L27
USPT	14 and 144	3	L26

USPT	l4 l44	0	L25
USPT	l23 not l4	0	L24
USPT	l4 and 84	3	L23
USPT	l21 not l4	0	L22
USPT	l4 and 49	4	L21
USPT	l19 not l4	0	L20
USPT	l4 and 16	22	L19
USPT	l15 not l4	0	L18
USPT	l4 and 188	9	L17
USPT	l4 near20 188	0	L16
USPT	l4 and 11	23	L15
USPT	l4 near10 188	0	L14
USPT	l4 near10 178	0	L13
USPT	l4 near10 169	0	L12
USPT	l4 near10 167	0	L11
USPT	l4 near10 144	0	L10
USPT	l4 near10 84	0	L9
USPT	l4 near10 49	0	L8
USPT	l4 near10 16	0	L7
USPT	l4 near10 11	0	L6
USPT	l1 and muta$4	507	L5
USPT	l1 near10 muta$4	23	L4
USPT	l1 near5 muta$4	23	L3
USPT	l1 near muta$4	4	L2
USPT	amylase near5 licheniformis	650	L1

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End of Result Set

Generate Collection

L17: Entry 9 of 9 File: USPT Apr 7, 1998

DOCUMENT-IDENTIFIER: US 5736499 A
TITLE: Mutant A-amylase

DEPR:
Residues corresponding to asparagine residues in .alpha.-amylase are identified herein for deletion or substitution. Thus, specific residues such as N188 refer to an amino acid position number (i.e., +188) which references the number assigned to the mature Bacillus lichenformis .alpha.-amylase sequence illustrated in FIG. 4. The invention, however, is not limited to the mutation of the particular mature .alpha.-amylase of Bacillus licheniformis but extends to precursor .alpha.-amylases containing amino acid residues at positions which are equivalent to the particular identified residue in Bacillus lichenformis .alpha.-amylase. A residue of a precursor .alpha.-amylase is equivalent to a residue of Bacillus licheniformis .alpha.-amylase if it is either homologous (i.e., corresponds in position for either the primary or tertiary structure) or analogous to a specific residue or portion of that residue in Bacillus lichenformis .alpha.-amylase (i.e., having the same or similar functional capacity to combine, react, or interact chemically or structurally).

DEPR:
The mutagenic primers were used as templates for the PCR primers PCR A+ and PCR B- resulting in a lengthened (61 bp) double stranded DNA. Each contained a different amino acid replacement at position 188, and all except N188M contained a different restriction site. Initially the PCR primers were annealed at 35.degree. C. for five minutes followed by a one minute DNA extension with tag polymerase at 75.degree. C. The double stranded DNA was then melted at 95.degree. C. for one minute, followed by the annealing and extension steps. Melting, annealing and extension continued for a total of 30 cycles.

DEPR:
DNA upstream and downstream of position 188 were made in separate PCR reactions. The template was pBLapr, and the PCR primers were LAAfs5 (SEQ ID NO:27) and PCR A- (SEQ ID NO:24) for upstream; and PCR B+(SEQ ID NO:25) and PCR Cla-Sall (SEQ ID NO:28) for downstream DNA. The DNA was melted at 95.degree. C. for one minute, annealed at 45.degree. C. for three minutes and elongated at 68.degree. C. for 3 minutes. The upstream portion is 290 bp and downstream is 498 bp. This procedure was repeated for 18 cycles using pfu polymerase. The same PCR procedure was used in steps (3) and (4).

DEPR:
Unique restriction sites, Asp718 and BssHII, are located upstream and downstream, respectively, of the 188 site. The final PCR product is digested with Asp718 and BssHII, the 333 bp fragment isolated by polyacrylamide gel electrophoresis and subcloned into the pHP.BL vector to obtain pHP.N188X.

DEPL:
Construction Of Plasmid Encoding .alpha.-Amylase Comprising Substitutions For Asparagine 188

WEST

Generate Collection

L4: Entry 4 of 23 File: USPT Apr 3, 2001

US-PAT-NO: 6211134
DOCUMENT-IDENTIFIER: US 6211134 B1

TITLE: Mutant .alpha.-amylase

DATE-ISSUED: April 3, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Caldwell; Robert M.	San Carlos	CA		
Mitchinson; Colin	Half Moon Bay	CA		
Ropp; Traci H	San Francisco	CA		

US-CL-CURRENT: 510/392; 510/226, 510/321, 510/330

CLAIMS:

We claim:
1. An .alpha.-amylase having a mutation corresponding to G475R in Bacillus licheniformis.
2. The .alpha.-amylase according to claim 1, wherein said mutation further comprises the deletion or substitution of a methionine or tryptophan residue.
3. The .alpha.-amylase according to claim 2, wherein said deletion or substitution of said methionine or tryptophan residue comprises a substitution or deletion corresponding to M15, W138 or M197 in Bacillus licheniformis.
4. The .alpha.-amylase according to claim 1 wherein said substitution further comprises the deletion or substitution of a residue corresponding to V128, H133, S187 or A209 in Bacillus licheniformis.
5. An .alpha.-amylase according to claim 1, wherein said substitution comprises a mutation corresponding to M15T/H133Y/S148N/N188S/A209V/A379S/G475R in Bacillus licheniformis.
6. The .alpha.-amylase according to claim 1, wherein said .alpha.-amylase is derived from Bacillus.
7. The .alpha.-amylase according to claim 6, wherein said .alpha.-amylase is derived from Bacillus licheniformis.
8. A DNA encoding the .alpha.-amylase according to claim 1.
9. A DNA encoding the .alpha.-amylase according to claim 3.
10. A DNA encoding the .alpha.-amylase according to claim 4.
11. A DNA encoding the .alpha.-amylase according to claim 5.
12. A DNA encoding the .alpha.-amylase according to claim 6.
13. An expression vector comprising the DNA of claim 9.
14. A host cell transformed with the expression vector of claim 13.
15. A detergent composition comprising the .alpha.-amylase according to claim 1.
16. The detergent composition according to claim 15, wherein said detergent is useful in laundering soiled fabric.
17. The detergent composition according to claim 15, wherein said detergent is useful in washing soiled dishes.

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Generate Collection

L17: Entry 3 of 9 File: USPT Nov 7, 2000

DOCUMENT-IDENTIFIER: US 6143708 A
TITLE: .alpha.-amylase mutants

BSPR:
It may be mentioned here that WO 96/23874 states that amino acid residues located within 10 .ANG. from a sodium or calcium ion are believed to be involved in, or of importance for, the Ca.sup.2+ binding capability of the enzyme, and that in this connection the mutation N104D [of the B. licheniformis .alpha.-amylase having the amino acid sequence shown in SEQ ID No. 2, or an equivalent (N to D) mutation of an equivalent position in another Termamyl-like .alpha.-amylase] is contemplated to be of particular interest with respect to decreasing the Ca.sup.2+ dependency of a Termamyl-like .alpha.-amylase.

BSPR:
In may be mentioned that in relation to achieving increased thermostability, WO 96/23874 discloses that a particularly interesting variant of a Termamyl-like .alpha.-amylase comprises a mutation corresponding to one of the following mutations (using the numbering of the B. licheniformis .alpha.-amylase amino acid sequence shown in SEQ ID NO 2):

BSPR:
The parent Termamyl-like .alpha.-amylase to be subjected to random mutagenesis according to the above principle may be any wild type .alpha.-amylase or a variant thereof containing one or more mutations. The parent may be a hybrid between at least two .alpha.-amylases as explained in further detail herein. Preferably, the parent .alpha.-amylase is a mutant of the B. licheniformis .alpha.-amylase having the sequence shown in SEQ ID No. 2 containing at least one mutation, and preferably multiple mutations. The parent .alpha.-amylase may alternatively be a hybrid .alpha.-amylase which contains at least a part of the B. licheniformis (SEQ ID No. 2) .alpha.-amylase. Specific examples of parent .alpha.-amylases suited to mutagenesis according to the above-described principles include: variants of the B. licheniformis (SEQ ID No. 2) .alpha.-amylase which contain at least one of, i.e. one, two, three, four or all five of, the mutations H156Y, A181T, N190F, A209V and Q264S; hybrid .alpha.-amylases which contain a part of the B. licheniformis (SEQ ID No. 2) .alpha.-amylase, preferably a C-terminal part thereof, such as amino acids 35-483 thereof, and a part of another Termamyl-like .alpha.-amylase such as B. amyloliquefaciens (SEQ ID No. 4) .alpha.-amylase, preferably an N-terminal part thereof such as the first 38 amino acid residues thereof.

BSPV:
(i) the .alpha.-amylase from B. licheniformis having the sequence shown in SEQ ID No. 2 with one or more variants (mutant .alpha.-amylases) according to the invention derived from (as the parent Termamyl-like .alpha.-amylase) the B. stearothermophilus .alpha.-amylase having the sequence shown in SEQ ID No. 6; or

BSPV:
(ii) the .alpha.-amylase from B. stearothermophilus having the sequence shown in SEQ ID No. 6 with one or more variants (mutant .alpha.-amylases) according to the invention derived from one or more other parent Termamyl-like .alpha.-amylases (e.g. from the B. licheniformis .alpha.-amylase having the sequence shown in SEQ ID No. 2, or from one of the other parent Termamyl-like .alpha.-amylases specifically referred to herein); or

BSPV:
(iii) one or more variants (mutant .alpha.-amylases) according to the invention derived from (as the parent Termamyl-like .alpha.-amylase) the B. stearothermophilus .alpha.-amylase having the sequence shown in SEQ ID No. 6 with one or more variants (mutant .alpha.-amylases) according to the invention derived from one or more other parent Termamyl-like .alpha.-amylases (e.g. from the B. licheniformis .alpha.-amylase having the sequence shown in SEQ ID No. 2, or from one of the other parent Termamyl-like .alpha.-amylases specifically referred to herein).

DEPL:
The mutations listed in the .alpha.-amylase list above are used to indicate variants of the B. licheniformis .alpha.-amylase (SEQ ID NO 2) (Termamyl) which has been modified by the indicated mutation(s).

DETL:
TABLE 2

Library DASII (Gln178-Asn192)

178
179 180 181 182 183 184 185 186 187 188 189 190 191 192 Gln Gly Lys Thr Trp Asp Trp Glu Val Ser Asn Glu Phe Gly Asn Primer: 5'CTG AAC CGC ATC TAT AAG TTT 1A2 34T AAG 567 TGG (SEQ ID No. 32) 89G GA10 GTT A11T 1213T GAA T1415 161718 AAC TAT GAT TAT TTG ATG TAT3'

WEST

Generate Collection

L17: Entry 3 of 9 File: USPT Nov 7, 2000

US-PAT-NO: 6143708
DOCUMENT-IDENTIFIER: US 6143708 A

TITLE: .alpha.-amylase mutants

DATE-ISSUED: November 7, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Svendsen; Allan	Birker.o slashed.d			DKX
Borchert; Torben Vedel	Jyllinge			DKX
Bisg.ang.rd-Frantzen; Henrik	Bagsv.ae butted.rd			DKX

ASSIGNEE-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY	TYPE CODE
Novo Nordisk A/S	Bagsv.ae butted.rd			DKX	03

APPL-NO: 9/ 182859
DATE FILED: October 29, 1998

PARENT-CASE:
CROSS-REFERENCE TO RELATED APPLICATIONS This application is a continuation of PCT/DK97/00197 filed Apr. 30, 1997 which claims priority under 35 U.S.C. 119 of Danish applications 0515/96 filed Apr. 30, 1996, 0712/96 filed Jun. 28, 1996, 0775/96 filed Jul. 11, 1996, and 1263/96 filed Nov. 8, 1996, the contents of which are fully incorporated herein by reference.

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	APPL-DATE
DK	0515/96	April 30, 1996
DK	0712/96	June 28, 1996
DK	0775/96	July 11, 1996
DK	1263/96	November 8, 1996

INT-CL: [7] C12N 9/28, C12N 1/20, C12N 15/00, C07H 21/04
US-CL-ISSUED: 510/226; 435/202, 435/252.3, 435/320.1, 536/23.2, 536/23.7, 510/326, 510/392
US-CL-CURRENT: 510/226; 435/202, 435/252.3, 435/320.1, 510/326, 510/392, 536/23.2, 536/23.7
FIELD-OF-SEARCH: 435/202, 435/252.3, 435/320.1, 510/226, 510/326, 510/392, 536/23.2, 536/23.7

PRIOR-ART-DISCLOSED:

U.S. PATENT DOCUMENTS

Search Selected Search ALL

	PAT-NO	ISSUE-DATE	PATENTEE-NAME	US-CL
☐	5731280	March 1998	Nielsen et al.	510/392
☐	5736499	April 1998	Michinson et al.	510/392
☐	5824532	October 1998	Barnett et al.	435/202

FOREIGN PATENT DOCUMENTS

FOREIGN-PAT-NO	PUBN-DATE	COUNTRY	US-CL
WO 91/00353	January 1991	WOX	
WO 95/10603	April 1995	WOX	
WO 95/35382	December 1995	WOX	
WO 96/23874	August 1996	WOX	

ART-UNIT: 162
PRIMARY-EXAMINER: Achutamurthy; Ponnathapu
ASSISTANT-EXAMINER: Saidha; Tekchand
ATTY-AGENT-FIRM: Zelson, Esq.; Steve T. Green, Esq.; Reza Lambiris, Esq.; Elias J.

ABSTRACT:

The invention relates to a variant of a parent Termamyl-like .alpha.-amylase, which variant has a-amylase activity and exhibits an alteration in at least one of the following properties relative to said parent a-amylase: substrate specificity, substrate binding, substrate cleavage pattern, thermal stability, pH/activity profile, pH/stability profile, stability towards oxidation, Ca.sup.2+ dependency and specific activity.

92 Claims, 3 Drawing figures

L26 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2001 ACS
AN 2001:161441 HCAPLUS
DN 134:190018
TI .alpha.-Amylase variants with improved detergent performance
IN Svendsen, Allan; Kjaerulff, Soeren; Bisgaard-Frantzen, Henrik; Andersen, Carsten
PA Novo-Nordisk A/S, Den.; Novo Alle
SO U.S., 36 pp.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6197565	B1	20010306	US 1998-193068	19981116

RE.CNT 2
RE
(1) Anon; DK WO9623874 1996
(2) Anon; DK WO9741213 1997

L26 ANSWER 2 OF 2 MEDLINE DUPLICATE 1
AN 2000438427 MEDLINE
DN 20425100 PubMed ID: 10966804
TI Probing structural determinants specifying high thermostability in Bacillus **licheniformis** alpha-**amylase**.
AU Declerck N; Machius M; Wiegand G; Huber R; Gaillardin C
CS Genetique Moleculaire et Cellulaire, INRA-UMR216 and CNRS-URA1925 INA-PG, Thiverval-Grignon, F-78850, France.. nathalie@tome.cbs.univ-montpl.fr
SO JOURNAL OF MOLECULAR BIOLOGY, (2000 Aug 25) 301 (4) 1041-57.
Journal code: J6V; 2985088R. ISSN: 0022-2836.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200009
ED Entered STN: 20000928
Last Updated on STN: 20000928
Entered Medline: 20000921

=> d kwic

L26 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2001 ACS
AB The invention relates to a variant of a parent Termamyl-like .alpha.-amylase, comprising **mutations** in two, three, four, five or six regions/positions. The variants have increased stability at high temps. (relative to the parent). The variants comprise addnl. **mutations** added to the LE174 hybrid .alpha.-enzyme in which the 35 N-terminal residues of Bacillus **licheniformis** .alpha.-**amylase** are replaced by residues 1-33 of BAN/B. amyloliquefaciens .alpha.-amylase. The invention also relates to a DNA construct comprising a DNA. . .
ST amylase variant **mutagenesis** stability sequence detergent
IT Bacillus (bacterium genus)
Bacillus amyloliquefaciens
Bacillus **licheniformis**
Bacillus stearothermophilus
Detergents
Mutagenesis
Protein engineering
Thermal stability
(.alpha.-**amylase** variants with improved detergent performance)
IT 84932-47-8DP, variants 98002-53-0DP, variants 115682-53-6DP, variants 167291-50-1DP, variants 171600-22-9DP, variants 171600-23-0DP, variants 171600-23-0P 199346-27-5DP, variants 326950-36-1DP, 1-33-Amylase, .alpha.- (Bacillus amyloliquefaciens gene amyQ) fusion protein with 36-483-.alpha.-amylase [156-tyrosine,174-arginine,181-

tyrosine,190-phenylalan[redacted]201-phenylalanine,205-asparag[redacted]209-valine,264-serine] (Bacillus licheniformis gene amyL) 326950-37-2P 326950-38-3P 326950-42-9P
RL: BPN (Biosynthetic preparation); MOA (Modifier or additive use); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; .alpha.-amylase variants with improved detergent performance)

=>